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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/085,167

DATE: 03/19/2002  
TIME: 16:12:54

Input Set : A:\99-29C1.txt  
Output Set: N:\CRF3\03192002\J085167.raw

3 <110> APPLICANT: Holloway, James L.  
4 Lok, Si  
6 <120> TITLE OF INVENTION: SECRETED PROTEIN ZACRP4  
8 <130> FILE REFERENCE: 99-29  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/085,167  
C--> 10 <141> CURRENT FILING DATE: 2002-02-27  
10 <150> PRIOR APPLICATION NUMBER: 60/141,928  
11 <151> PRIOR FILING DATE: 1999-07-01  
14 <160> NUMBER OF SEQ ID NOS: 9  
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 1357  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
23 <220> FEATURE:  
24 <221> NAME/KEY: CDS  
25 <222> LOCATION: (210)...(1196)  
27 <400> SEQUENCE: 1  
28 cgcccgcccc ctgccccag caccctgtcc gctgccgcct cagagccggg aaaagcagcc 60  
29 ggagcccccg ccgccccctgc cgcagcgcg gcggtcagcg cgcagcccg caccgcagc 120  
30 ctgcagcctg cagccccgag cccgcagccc ggagccagat cgcgggctca gaccgaaccc 180  
31 gactcgaccg ccgccccag ccaggcgcc atg ctg ccg ctt ctg ctg ggc ctg 233  
32 Met Leu Pro Leu Leu Leu Gly Leu  
33 1 5  
35 ctg ggc cca gcg gcc tgc tgg gcc ctg ggc ccg acc ccc ggc ccg gga 281  
36 Leu Gly Pro Ala Ala Cys Trp Ala Leu Gly Pro Thr Pro Gly Pro Gly  
37 10 15 20  
39 tcc tct gag ctg cgc tcg gcc ttc tcg gcg gca cgc acc acc ccc ctg 329  
40 Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro Leu  
41 25 30 35 40  
43 gag ggc acg tcg gag atg gcg gtg acc ttc gac aag gtg tac gtg aac 377  
44 Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys Val Tyr Val Asn  
45 45 50 55  
47 atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt cgc tgc cgc gtg 425  
48 Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg Val  
49 60 65 70  
51 ccc ggc gcc tac ttc ttc tcc ttc acg gct ggc aag gcc ccg cac aag 473  
52 Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His Lys  
53 75 80 85  
55 agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag gtg cag gcg ctg 521  
56 Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala Leu  
57 90 95 100  
59 gcc ttc gac gag cag cgg cgg cca gcc gcg cgg cgc gca gcc agc cag 569

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```

60  Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser Gln
61  105                               110                               115                               120
63  agc gcc atg ctg cag ctc gac tac ggc gac aca gtg tgg ctg cgg ctg      617
64  Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu
65                               125                               130                               135
67  cat ggc gcc ccg cac tac gcg cta ggc gcg ccc ggc gcc acc ttc agc      665
68  His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser
69                               140                               145                               150
71  ggc tac cta gtc tac gcc gac gcc gac gct gac gcg cct gcg cgc ggg      713
72  Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Pro Ala Arg Gly
73                               155                               160                               165
75  ccg ccc gcg ccc ccc gag ccg cgc tcg gcc ttc tcg gcg gcg cgc acg      761
76  Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr
77  170                               175                               180
79  cgc agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg cgg cac caa cca      809
80  Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro Arg His Gln Pro
81  185                               190                               195                               200
83  ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc gac ttc gac gcg      857
84  Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly Asp Phe Asp Ala
85                               205                               210                               215
87  gcg gcc ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc tac ttc ttc tcc      905
88  Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser
89                               220                               225                               230
91  ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg gtt aag ctg atg      953
92  Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met
93  235                               240                               245
95  aag aac cgc gac gag gtg cag gcc atg att tac gac gac ggc gcg tcg      1001
96  Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser
97  250                               255                               260
99  cgg cgc cgc gag atg cag agc cag agc gtg atg ctg gcc ctg cgg cgc      1049
100 Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu Ala Leu Arg Arg
101 265                               270                               275                               280
103 ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac ggc tac ggc gcc      1097
104 Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala
105                               285                               290                               295
107 tac agc aac cac ggc aag tac atc acc ttc tcc ggc ttc ctg gtg tac      1145
108 Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr
109                               300                               305                               310
111 ccc gac ctc gcc ccc gcc gcc ccg ccg ggc ctc ggg gcc tcg gag cta      1193
112 Pro Asp Leu Ala Pro Ala Ala Pro Pro Gly Leu Gly Ala Ser Glu Leu
113 315                               320                               325
115 ctg tgagccccgg gccagagaag agccccgggag ggccaggggc gtgcatgcc      1246
116 Leu
118 ggccggggccc gaggctcgaa agtcccgccg gagcgccacg gcctccgggc gcgcctggac      1306
119 tctgccaata aagcggaaag cgggcacgcg cagcggcccg cagcccaggc a      1357
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 329
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens

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```

126 <400> SEQUENCE: 2
127 Met Leu Pro Leu Leu Leu Gly Leu Leu Gly Pro Ala Ala Cys Trp Ala
128 1 5 10 15
129 Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe
130 20 25 30
131 Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val
132 35 40 45
133 Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala
134 50 55 60
135 Thr Gly Gln Phe Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe
136 65 70 75 80
137 Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg
138 85 90 95
139 Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro
140 100 105 110
141 Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr
142 115 120 125
143 Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu
144 130 135 140
145 Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala
146 145 150 155 160
147 Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg
148 165 170 175
149 Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala
150 180 185 190
151 Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val
152 195 200 205
153 Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg
154 210 215 220
155 Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg
156 225 230 235 240
157 Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala
158 245 250 255
159 Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln
160 260 265 270
161 Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser
162 275 280 285
163 His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile
164 290 295 300
165 Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro
166 305 310 315 320
167 Pro Gly Leu Gly Ala Ser Glu Leu Leu
168 325
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 31
172 <212> TYPE: PRT
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Clq Aromatic Motif

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```

178 <221> NAME/KEY: VARIANT
179 <222> LOCATION: (2)...(6)
180 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
182 <221> NAME/KEY: VARIANT
183 <222> LOCATION: (7)...(7)
184 <223> OTHER INFORMATION: Xaa is asparagine or aspartic acid
186 <221> NAME/KEY: VARIANT
187 <222> LOCATION: (8)...(11)
188 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
190 <221> NAME/KEY: VARIANT
191 <222> LOCATION: (12)...(12)
192 <223> OTHER INFORMATION: Xaa is phenylalanine, tyrosine, tryptophan or
193     leucine
196 <221> NAME/KEY: VARIANT
197 <222> LOCATION: (13)...(18)
198 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
200 <221> NAME/KEY: VARIANT
201 <222> LOCATION: (20)...(24)
202 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
204 <221> NAME/KEY: VARIANT
205 <222> LOCATION: (26)...(26)
206 <223> OTHER INFORMATION: Xaa is any amino acid residue
208 <221> NAME/KEY: VARIANT
209 <222> LOCATION: (28)...(28)
210 <223> OTHER INFORMATION: Xaa is any amino acid residue
212 <221> NAME/KEY: VARIANT
213 <222> LOCATION: (30)...(30)
214 <223> OTHER INFORMATION: Xaa is any amino acid residue
216 <221> NAME/KEY: VARIANT
217 <222> LOCATION: (31)...(31)
218 <223> OTHER INFORMATION: Xaa is phenylalanine or tyrosine
220 <400> SEQUENCE: 3
W--> 221  Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      222    1             5             10             15
W--> 223  Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
      224             20             25             30
226 <210> SEQ ID NO: 4
227 <211> LENGTH: 987
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Degenerate nucleotide sequence encoding the
233     polypeptide of SEQ ID NO:2
235 <221> NAME/KEY: variation
236 <222> LOCATION: (1)...(987)
237 <223> OTHER INFORMATION: Each N is A, T, G or C
239 <400> SEQUENCE: 4
W--> 240  atgytnccny tnytnytnngg nytnytnngn ccngcngcnt gytgggcnyt nggnccnacb      60
W--> 241  ccnggnccng gnwsnwsnga rytngnwnsn gcnttywsng cngcnmgnac nacnccnytn      120

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```

W--> 242 garggnacnw sngaratggc ngtnacntty gayaargtnt aygtnaayat hggnggngay 180
W--> 243 ttygaygtng cnacongncn rttymgntgy mgngtnccng gngcntaytt yttywsntty 240
W--> 244 acngcnggna argcnccnca yaarwsnytn wsngtnatgy tngtnmgnaa ymgngaygar 300
W--> 245 gtncargcny tngcnttyga ygarcarmgn mgncnggng cnmgnmgngc ngcnwsncar 360
W--> 246 wsngcnatgy tncarytnga ytayggngay acngtntggy tnmgnytnca yggngcnccn 420
W--> 247 caytaygcn y tngngcncc nggngcnacn ttywsngnt ayytngnta ygcngaygc 480
W--> 248 gaygcngayg cncngcnmg nggncnccn gcncncncng arcnmgnws ngcnttywsn 540
W--> 249 gcngcnmgna cnmgnwsnyt ngtnngnwsn gaygcnggnc cnggncnmg ncaycarccn 600
W--> 250 ytngcnttyg ayacngartt ygtnaayath ggnggngayt tygaygcngc ngcnggngtn 660
W--> 251 ttymgntgym gnytnccng ngcntaytty ttywsnttya cnytnngnaa rytncnmg 720
W--> 252 aaracnytnw sngtnaaryt natgaaraay mgngaygarg tncargcnat gathtaygay 780
W--> 253 gayggngcnw snmgngnmgn ngaratgcar wsncarwsng tnatgytngc nytnmgngmgn 840
W--> 254 ggngaygcng tntggytnyt nwsncaygay caygayggnt ayggngenta ywsnaaycay 900
W--> 255 ggnaartaya thacnttyws nggnttyytn gntayccng ayytngcncc ngcngcnccn 960
W--> 256 ccnggnytn gngcnwsnga rytntn 987

258 <210> SEQ ID NO: 5
259 <211> LENGTH: 24
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Oligonucleotide ZC20,839
266 <400> SEQUENCE: 5 24
267 atgtacttgc cgtggttgc gtag
269 <210> SEQ ID NO: 6
270 <211> LENGTH: 23
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Oligonucleotide ZC20840
277 <400> SEQUENCE: 6 23
278 cgacaccgag ttcgtcaaca ttg
280 <210> SEQ ID NO: 7
281 <211> LENGTH: 325
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Degenerate nucleotide sequence encoding the
287 polypeptide of SEQ ID NO:2.
289 <221> NAME/KEY: variation
290 <222> LOCATION: (1)...(325)
291 <223> OTHER INFORMATION: Each N is independently A, T, C or G.
294 <400> SEQUENCE: 7
295 ctggccccgg gccgcggcac caaccactcg ccttcgacac cgagttcgtc aacattggcg 60
W--> 296 gcgacttcga cgcggcgccc ggcgtgttcc gctgccgtct gnccggcgcc tacttcttct 120
W--> 297 ncttcacgct gggcaagctg ccgcgtaaga cgtgtcgggt taagctgatg aagaaccgcg 180
298 acgaggtgca ggccatgatt tacgacgacg gcgcgtcgcg gcgccgcgag atgcagagcc 240
W--> 299 agagcgtgat gctggccctg cggcgcgng acgccgtctg gctgtcagcc acgaccacga 300
300 cggctacggc gcctacagca accac 325
302 <210> SEQ ID NO: 8

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/085,167

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Input Set : A:\99-29C1.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7